

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

SAVERIO CARL FALCO ET AL.

CASE NO.: BB1126 USDIV

APPLICATION NO.: UNKNOWN

GROUP ART UNIT: UNKNOWN

FILED: HEREWITH

EXAMINER: UNKNOWN

FOR: PLANT BRANCHED-CHAIN AMINO ACID
BIOSYNTHETIC ENZYME**PRELIMINARY AMENDMENT**Commissioner for Patents
Washington, DC 20231

Sir:

Prior to examination, please amend the captioned application as follows and consider the following remarks.

IN THE SPECIFICATION:**Please replace the following paragraphs:****Paragraph beginning at page 1, line 3:**

This application is a divisional application of U.S. Application No. 09/173,300, filed October 15, 1998, which claims the benefit of U.S. Provisional Application No. 60/063,423, filed October 28, 1997.

Paragraph beginning at page 4, line 7:

Figure 2 (A-C) depicts the amino acid sequence alignments between the dihydroxyacid dehydratase from corn clone cr1.pk0032.c4 (SEQ ID NO:2), soybean contig assembled from clones se3.pk0006.g4, and ses9c.pk001.o8 (SEQ ID NO:4), wheat clone wkm2c.pk005.c12 (SEQ ID NO:6), and *Saccharomyces cerevisiae* (NCBI gi Accession No. 1170543, SEQ ID NO:7). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 13:

Figure 3 (A-C) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from corn clone cc71se-b.pk0008.b5 (SEQ ID NO:9), corn clone cen6.pk0003.b5 (SEQ ID NO:11), corn clone cta1n.pk0070.e7 (SEQ ID NO:13), rice clone rls24.pk0025.f6 (SEQ ID NO:15), soybean clone ses8w.pk0032.e9 (SEQ ID NO:17), wheat clone wlm96.pk027.n2 (SEQ ID NO:19), and *Bacillus subtilis* (NCBI gi Accession No. 1706292, SEQ ID NO:20). Amino acids which are conserved among all sequences are

indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 21:

Figure 4 (A-B) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from rice clone rls72.pk0014.a3 (SEQ ID NO:22), soybean clone sre.pk0001.d1 (SEQ ID NO:24), soybean clone srr2c.pk003.d20 (SEQ ID NO:26), wheat clone wl1n.pk0123.c11 (SEQ ID NO:28), and *Methanococcus jannaschii* (NCBI gi Accession No. 124380, SEQ ID NO:29). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 28:

Figure 5 (A-B) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from corn clone cco1.pk0030.d2 (SEQ ID NO:31), wheat clone wkm1c.pk0004.c7 (SEQ ID NO:33), and *Escherichia coli* (NCBI gi Accession No. 1705437, SEQ ID NO:34). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 34:

Figure 6 (A-C) depicts the amino acid sequence alignments between the *leuC* subunit of 3-isopropylmalate dehydratase from the corn contig assembled from clones cen1.pk0032.b1, cta1n.pk0077.c7, cen3n.pk0015.g3, cen3n.pk0060.h4, and cen3n.pk0121.h11 (SEQ ID NO:36), corn clone cr1n.pk0153.e9 (SEQ ID NO:38), rice clone rl0n.pk087.k16 (SEQ ID NO:40), soybean contig assembled from clones sd3c.pk008.k13, and srm.pk0006.h5 (SEQ ID NO:42), wheat clone wre1n.pk0045.b10 (SEQ ID NO:44), and *Rhizomucor pusillus* (NCBI gi Accession No. 1708799, SEQ ID NO:45). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 5, line 5:

Figure 7 (A-B) depicts the amino acid sequence alignments between the *leuD* subunit of 3-isopropylmalate dehydratase from corn clone cr1n.pk0123.b7 (SEQ ID NO:47), rice clone rls12.pk0001.c2 (SEQ ID NO:49), soybean clone srr1c.pk003.c2 (SEQ ID NO:51), wheat clone wl1n.pk0048.a6 (SEQ ID NO:53), and *Lactococcus lactis* (NCBI gi Accession No. 400187, SEQ ID NO:54). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

IN THE CLAIMS:

Please cancel claims 1-26. Please add the following claims:

27. "added" An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide having leuD activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:47, 49, 51, or 53 have at least 80% sequence identity based on the Clustal alignment method, or

(b) the complement of the nucleotide sequence, wherein the complement and the nucleotide sequence contain the same number of nucleotides and are 100% complementary.

28. "added" The polynucleotide of Claim 27 wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:47, 49, 51, or 53 have at least 90% sequence identity based on the Clustal alignment method.

29. "added" The polynucleotide of Claim 27 wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:47, 49, 51, or 53 have at least 95% sequence identity based on the Clustal alignment method.

30. "added" The polynucleotide of Claim 27 wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:47, 49, 51, or 53.

31. "added" The polynucleotide of claim 27 wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:46, 48, 50, or 52.

32. "added" A vector comprising the polynucleotide of Claim 27.

33. "added" A recombinant DNA construct comprising the polynucleotide of Claim 27 operably linked to a regulatory sequence.

34. "added" A method for transforming a cell comprising transforming a cell with the polynucleotide of Claim 27.

35. "added" A cell comprising the recombinant DNA construct of Claim 33.

36. "added" A method for producing a plant comprising transforming a plant cell with the polynucleotide of Claim 27 and regenerating a plant from the transformed plant cell.

37. "added" A plant comprising the recombinant DNA construct of Claim 33.

38. "added" A seed comprising the recombinant DNA construct of Claim 33.

39. "added" An isolated polynucleotide comprising a first nucleotide sequence, wherein the first nucleotide sequence contains at least 30 nucleotides, and wherein the first nucleotide sequence is comprised by another polynucleotide, wherein the other polynucleotide includes:

(a) a second nucleotide sequence, wherein the second nucleotide sequence encodes a polypeptide having leuD activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:47, 49, 51, or 53 have at least 80% sequence identity based on the Clustal alignment method, or

(b) the complement of the second nucleotide sequence, wherein the complement and the second nucleotide sequence contain the same number of nucleotides and are 100% complementary.

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40. "added" A method for isolating a polypeptide encoded by the polynucleotide of Claim 27 comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide operably linked to a regulatory sequence.


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REMARKS

Claims 1-26 have been canceled and claims 27-40 added. The newly added claims are drawn to the invention of Group VII (nucleic acid encoding leuD subunit of 3-isopropylmalate dehydratase (hydro-lyase) and host cell) of the restriction requirement mailed March 29, 2000 in the parent application, U.S. Application No. 09/173,300. No new matter is added by the addition of claims 27-40.

Entry of the amendments and favorable consideration of the claims are respectfully requested.

Respectfully submitted,



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Dated: December 20, 2001

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown as brackets, and inserted material is shown underlined.

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Claims 27-40 added.

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